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RAW SEQUENCE LISTING  
PATENT APPLICATION US/08/572,027DATE: 02/14/96  
TIME: 17:56:58

INPUT SET: S8732.raw

This Raw Listing contains the General  
Information Section and up to the first 5 pages.

## SEQUENCE LISTING

ENTERE

## (1) General Information:

(i) APPLICANT: DeBonte, L. et al.

(ii) TITLE OF INVENTION: PLANTS HAVING MUTANT SEQUENCES THAT CONFER  
ALTERED FATTY ACID PROFILES

(iii) NUMBER OF SEQUENCES: 8

## (iv) CORRESPONDENCE ADDRESS:

- (A) ADDRESSEE: Fish & Richardson, P.C., P.A.
- (B) STREET: 60 South Sixth Street, Suite 3300
- (C) CITY: Minneapolis
- (D) STATE: MN
- (E) COUNTRY: USA
- (F) ZIP: 55402

## (v) COMPUTER READABLE FORM:

- (A) MEDIUM TYPE: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30

## (vi) CURRENT APPLICATION DATA:

- (A) APPLICATION NUMBER:
- (B) FILING DATE:
- (C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 08/416,497
- (B) FILING DATE: 04-APR-1995

- (A) APPLICATION NUMBER: US 08/170,886
- (B) FILING DATE: 21-DEC-1993

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/739,965
- (B) FILING DATE: 05-AUG-1991
- (C) CLASSIFICATION:

## (vi) PRIOR APPLICATION DATA:

- (A) APPLICATION NUMBER: US 07/575,542
- (B) FILING DATE: 30-AUG-1990

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PATENT APPLICATION US/08/572,027DATE: 02/14/96  
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47 (C) CLASSIFICATION:  
48  
49 (viii) ATTORNEY/AGENT INFORMATION:  
50 (A) NAME: Ellinger, Mark S.  
51 (B) REGISTRATION NUMBER: 34,812  
52 (C) REFERENCE/DOCKET NUMBER: A21-535.10  
53  
54 (ix) TELECOMMUNICATION INFORMATION:  
55 (A) TELEPHONE: 612/335-5070  
56 (B) TELEFAX: 612/288-9696  
57  
58 (2) INFORMATION FOR SEQ ID NO:1:  
59  
60 (i) SEQUENCE CHARACTERISTICS:  
61 (A) LENGTH: 1155 base pairs  
62 (B) TYPE: nucleic acid  
63 (C) STRANDEDNESS: single  
64 (D) TOPOLOGY: linear  
65  
66 (ii) MOLECULE TYPE: DNA  
67  
68 (iii) HYPOTHETICAL: NO  
69  
70 (iv) ANTI-SENSE: NO  
71  
72 (vi) ORIGINAL SOURCE:  
73 (A) ORGANISM: Brassica napus  
74  
75 (ix) FEATURE:  
76 (D) OTHER INFORMATION: Wild type D form.  
77  
78  
79 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:  
80  
81 ATG GGT GCA GGT GGA AGA ATG CAA GTG TCT CCT CCC TCC AAG AAG TCT 48  
82 Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser  
83 1 5 10 15  
84  
85 GAA ACC GAC ACC ATC AAG CGC GTA CCC TGC GAG ACA CCG CCC TTC ACT 96  
86 Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr  
87 20 25 30  
88  
89 GTC GGA GAA CTC AAG AAA GCA ATC CCA CCG CAC TGT TTC AAA CGC TCG 144  
90 Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser  
91 35 40 45  
92  
93 ATC CCT CGC TCT TTC TCC TAC CTC ATC TGG GAC ATC ATC ATA GCC TCC 192  
94 Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser  
95 50 55 60  
96  
97 TGC TTC TAC TAC NTC GCC ACC ACT TAC TTC CCT CTC CTC CCT CAC CCT 240  
98 Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro  
99 65 70 75 80

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100																		
101	CTC	TCC	TAC	TTC	GCC	TGG	CCT	CTC	TAC	TGG	GCC	TGC	CAA	GGG	TGC	GTC		288
102	Leu	Ser	Tyr	Phe	Ala	Trp	Pro	Leu	Tyr	Trp	Ala	Cys	Gln	Gly	Cys	Val		
103					85					90					95			
104																		
105	CTA	ACC	GGC	GTC	TGG	GTC	ATA	GCC	CAC	GAA	TGC	GGC	CAC	CAC	GCC	TTC		336
106	Leu	Thr	Gly	Val	Trp	Val	Ile	Ala	His	Glu	Cys	Gly	His	His	Ala	Phe		
107				100					105					110				
108																		
109	AGC	GAC	TAC	CAG	TGG	CTT	GAC	GAC	ACC	GTC	GGT	CTC	ATC	TTC	CAC	TCC		384
110	Ser	Asp	Tyr	Gln	Trp	Leu	Asp	Asp	Thr	Val	Gly	Leu	Ile	Phe	His	Ser		
111			115				120						125					
112																		
113	TTC	CTC	CTC	GTC	CCT	TAC	TTC	TCC	TGG	AAG	TAC	AGT	CAT	CGC	AGC	CAC		432
114	Phe	Leu	Leu	Val	Pro	Tyr	Phe	Ser	Trp	Lys	Tyr	Ser	His	Arg	Ser	His		
115		130				135						140						
116																		
117	CAT	TCC	AAC	ACT	GGC	TCC	CTC	GAG	AGA	GAC	GAA	GTG	TTT	GTC	CCC	AAG		480
118	His	Ser	Asn	Thr	Gly	Ser	Leu	Glu	Arg	Asp	Glu	Val	Phe	Val	Pro	Lys		
119	145					150					155					160		
120																		
121	AAG	AAG	TCA	GAC	ATC	AAG	TGG	TAC	GGC	AAG	TAC	CTC	AAC	AAC	CCT	TTG		528
122	Lys	Lys	Ser	Asp	Ile	Lys	Trp	Tyr	Gly	Lys	Tyr	Leu	Asn	Asn	Pro	Leu		
123					165					170					175			
124																		
125	GGA	CGC	ACC	GTG	ATG	TTA	ACG	GTT	CAG	TTC	ACT	CTC	GGC	TGG	CCG	TTG		576
126	Gly	Arg	Thr	Val	Met	Leu	Thr	Val	Gln	Phe	Thr	Leu	Gly	Trp	Pro	Leu		
127				180					185					190				
128																		
129	TAC	TTA	GCC	TTC	AAC	GTC	TCG	GGA	AGA	CCT	TAC	GAC	GGC	GGC	TTC	CGT		624
130	Tyr	Leu	Ala	Phe	Asn	Val	Ser	Gly	Arg	Pro	Tyr	Asp	Gly	Gly	Phe	Arg		
131			195					200					205					
132																		
133	TGC	CAT	TTC	CAC	CCC	AAC	GCT	CCC	ATC	TAC	AAC	GAC	CGC	GAG	CGT	CTC		672
134	Cys	His	Phe	His	Pro	Asn	Ala	Pro	Ile	Tyr	Asn	Asp	Arg	Glu	Arg	Leu		
135		210				215						220						
136																		
137	CAG	ATA	TAC	ATC	TCC	GAC	GCT	GGC	ATC	CTC	GCC	GTC	TGC	TAC	GGT	CTC		720
138	Gln	Ile	Tyr	Ile	Ser	Asp	Ala	G										

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153  GAT TGG TTC AGG GGA GCT TTG GCT ACC GTT GAC AGA GAC TAC GGA ATC      912
154  Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
155      290                      295                      300
156
157  TTG AAC AAG GTC TTC CAC AAT ATT ACC GAC ACG CAC GTG GCC CAT CAT      960
158  Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
159  305                      310                      315                      320
160
161  CCG TTC TCC ACG ATG CCG CAT TAT CAC GCG ATG GAA GCT ACC AAG GCG      1008
162  Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
163      325                      330                      335
164
165  ATA AAG CCG ATA CTG GGA GAG TAT TAT CAG TTC GAT GGG ACG CCG GTG      1056
166  Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
167      340                      345                      350
168
169  GTT AAG GCG ATG TGG AGG GAG GCG AAG GAG TGT ATC TAT GTG GAA CCG      1104
170  Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
171      355                      360                      365
172
173  GAC AGG CAA GGT GAG AAG AAA GGT GTG TTC TGG TAC AAC AAT AAG TTA T      1153
174  Asp Arg Gln Gly Glu Lys Lys Gly Val Phe Trp Tyr Asn Asn Lys Leu
175      370                      375                      380
176
177  GA      1155
178
179
180  (2) INFORMATION FOR SEQ ID NO:2:
181
182      (i) SEQUENCE CHARACTERISTICS:
183          (A) LENGTH: 384 amino acids
184          (B) TYPE: amino acid
185          (D) TOPOLOGY: linear
186
187      (ii) MOLECULE TYPE: protein
188
189      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:
190
191  Met Gly Ala Gly Gly Arg Met Gln Val Ser Pro Pro Ser Lys Lys Ser
192      1                      5                      10                      15
193
194  Glu Thr Asp Thr Ile Lys Arg Val Pro Cys Glu Thr Pro Pro Phe Thr
195      20                      25                      30
196
197  Val Gly Glu Leu Lys Lys Ala Ile Pro Pro His Cys Phe Lys Arg Ser
198      35                      40                      45
199
200  Ile Pro Arg Ser Phe Ser Tyr Leu Ile Trp Asp Ile Ile Ile Ala Ser
201      50                      55                      60
202
203  Cys Phe Tyr Tyr Xaa Ala Thr Thr Tyr Phe Pro Leu Leu Pro His Pro
204      65                      70                      75                      80
205

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206  Leu Ser Tyr Phe Ala Trp Pro Leu Tyr Trp Ala Cys Gln Gly Cys Val
207              85                      90                      95
208
209  Leu Thr Gly Val Trp Val Ile Ala His Glu Cys Gly His His Ala Phe
210              100                      105                      110
211
212  Ser Asp Tyr Gln Trp Leu Asp Asp Thr Val Gly Leu Ile Phe His Ser
213              115                      120                      125
214
215  Phe Leu Leu Val Pro Tyr Phe Ser Trp Lys Tyr Ser His Arg Ser His
216              130                      135                      140
217
218  His Ser Asn Thr Gly Ser Leu Glu Arg Asp Glu Val Phe Val Pro Lys
219  145                      150                      155                      160
220
221  Lys Lys Ser Asp Ile Lys Trp Tyr Gly Lys Tyr Leu Asn Asn Pro Leu
222              165                      170                      175
223
224  Gly Arg Thr Val Met Leu Thr Val Gln Phe Thr Leu Gly Trp Pro Leu
225              180                      185                      190
226
227  Tyr Leu Ala Phe Asn Val Ser Gly Arg Pro Tyr Asp Gly Gly Phe Arg
228              195                      200                      205
229
230  Cys His Phe His Pro Asn Ala Pro Ile Tyr Asn Asp Arg Glu Arg Leu
231              210                      215                      220
232
233  Gln Ile Tyr Ile Ser Asp Ala Gly Ile Leu Ala Val Cys Tyr Gly Leu
234  225                      230                      235                      240
235
236  Phe Arg Tyr Ala Ala Gly Gln Gly Val Ala Ser Met Val Cys Phe Tyr
237              245                      250                      255
238
239  Gly Val Pro Leu Leu Ile Val Asn Gly Phe Leu Val Leu Ile Thr Tyr
240              260                      265                      270
241
242  Leu Gln His Thr His Pro Ser Leu Pro His Tyr Asp Ser Ser Glu Trp
243              275                      280                      285
244
245  Asp Trp Phe Arg Gly Ala Leu Ala Thr Val Asp Arg Asp Tyr Gly Ile
246              290                      295                      300
247
248  Leu Asn Lys Val Phe His Asn Ile Thr Asp Thr His Val Ala His His
249  305                      310                      315                      320
250
251  Pro Phe Ser Thr Met Pro His Tyr His Ala Met Glu Ala Thr Lys Ala
252              325                      330                      335
253
254  Ile Lys Pro Ile Leu Gly Glu Tyr Tyr Gln Phe Asp Gly Thr Pro Val
255              340                      345                      350
256
257  Val Lys Ala Met Trp Arg Glu Ala Lys Glu Cys Ile Tyr Val Glu Pro
258              355                      360                      365

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**SEQUENCE VERIFICATION REPORT**  
PATENT APPLICATION *US/08/572,027*

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Original Text